

114 Sequence Listing.ST25.txt
SEQUENCE LISTING

<110> Rodríguez Aguirre, José Francisco
González De Llano, Ma Dolores
Oña Blanco, Ana María
Abaitua Elustondo, Fernando
Maraver Molina, Antonio
Clemente Cervera, Roberto
Ruiz Castón, José
Rodríguez Fernández-Alba, Juan Ramón

<120> WHOLE EMPTY VIRAL PARTICLES OF THE INFECTIOUS BURSAL DISEASE
VIRUS (IBDV), PRODUCTION PROCESS AND APPLICATIONS

<130> 4258-114

<140> Not yet assigned

<141> 2005-09-30

<150> P200300751

<151> 2003-03-31

<150> PCT/ES2004/000147

<151> 2004-03-31

<160> 9

<170> PatentIn version 3.3

<210> 1

<211> 10909

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> gene

<222> (3)..(3041)

<223> Open reading frame of IBDV polyprotein in reverse complementary strand

<220>

<221> promoter

<222> (3083)..(3211)

<223> AcMNV polyhedrin promoter

<220>

<221> promoter

<222> (3230)..(3351)

<223> AcMNV p10 promoter

<220>

<221> CDS

<222> (3388)..(6027)

<223> Open reading frame of IBDV VP1 protein

<220>

<221> polyA_site

<222> (6068)..(6331)

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<220>
 <221> gene
 <222> (6901)..(7434)
 <223> Gentamicin resistance gene

<220>
 <221> misc_feature
 <222> (7501)..(7725)
 <223> Minitransposon Tn7R

<220>
 <221> gene
 <222> (8787)..(9647)
 <223> Ampicillin resistance gene

<220>
 <221> misc_feature
 <222> (9854)..(10234)
 <223> F1

<220>
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 <222> (10418)..(10583)
 <223> Minitransposon Tn7L

<400> 1
 gctcactcaa ggtcctcatc agagacggtc ctgatccagc ggcccagccg accagggggt 60
 ctctgtgttg gagcattggg ttttggttgg ggcttttggt gagcccgctt gggattgcga 120
 tgcttcatct ccatcgcagt caagagcaga tctttcatct gttcttggtt tgggccacgt 180
 ccatggttga tttcatagac tttggcaact tcgtctatga aagcttgggg tggctctgcc 240
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 cggtctttct ctgcatgcac gtagtctaga tagtcctcgt ttgggtccgg tatttctcgt 360
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 cattctggtg ttgcaaagta gatgcccatt gtctccatct tctttgagat ccgtgtgtct 480
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 atccgatggg cgttcgggtc gctgagtgcg aagttggcca tgtcagtcac aatcccatc 660
 tcttccagcc acatgaacac actgagtgcg gattggaata gtgggtccac gttggctgct 720
 gcttccattg ctctgacggc actctcgagt tcgggggtct ctttgaactc tgatgcagcc 780
 atggcaaggt ggtactggcg tcctgcattg ggtggaaggt atggtagggt gaggtagggg 840
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 ccggtgttta catcgaatgc tccgggacca gccaacctaa ggccaagtcg gtgtgcagta 960
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 gtcatagcc catggattgg gactttgggt cgaaacacat ccatgtaagc tatggctaga 1080
 tttccactgt ttcccacaat aggaggtatg ggatcttttg acagcataat gctgtcgtcc 1140

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| | |
|--|------|
| cagacatcat ctattgggac aacgggtgtag tctctcccag tctccagtgg aagtacccca | 1200 |
| tctggagcat atccatagac tctgtgtcca gagagagttc gtatgaagga tcctctttga | 1260 |
| gatggagggt ggaggtcttc tcgcacgcct tcaatgacag caaacatttt gctgttcaat | 1320 |
| gctttgggtg tcatggcgtc ttccactgtc gtaataacca cagggaaatag cgtggcaccc | 1380 |
| tctcttaaca cgcagtcgag gttgtgtgca ccgcggagta cccaggtga agcaagaatc | 1440 |
| ccgtcgacta cgggattctg gggcacctgg aatagattcg cgactacctc gtacccttg | 1500 |
| tcggcggcga gagtcagctg ccttatgcgg cctgaggcag ctcttgcttt tcctgacgcg | 1560 |
| gctcgagcag ttctgaagc ggcctgggcc tcatcgccca gcaggtagtc tacaccttc | 1620 |
| ccaattgcat gggctagggg agcggcaggt gggaacaatg tggagaccac cggcacagct | 1680 |
| atcctcctta tggcccgat tatgtctttg aagccgaatg ctctgcaat cttcagggga | 1740 |
| gagttgaggt cggccacctc catgaagtat tcacgaaagt cagtgtactc cttgtttggc | 1800 |
| cagacggtct tgatgccaaag acggtccctc tcaactagta tcaattttgt gtagttcatg | 1860 |
| gctcctgggt caaatcggcc gtattctgta accaggttct ttgctagttc aggatttggg | 1920 |
| atcagctcga agttgctcac ccagcgacc gtaacgacgg atcctgttgc cactctttcg | 1980 |
| taggccacta gcgtgacggg acggagggcc cctggatagt tgccaccatg gatcgtcact | 2040 |
| gctaggctcc ctcttgccga ccatgacatc tgatcccctg cctgaccacc acttttggag | 2100 |
| gtcactatct ccagtttgat ggatgtgatt ggctgggtta tctcgtttgt tggaatcaca | 2160 |
| agattgaatg gcataagggt gtcggtgccg gtcgtcagcc cattgtttgc ggccacagcc | 2220 |
| ctggtgatta ccgttgtccc atcaaagcct atgaggtaga tgggtggcgcc cagtacaagg | 2280 |
| ccgtggacgc ttgttcgaaa cacgagctct cccccaacgc tgaggcttgt gatggcatca | 2340 |
| atgttggtcg agaacagtgt gattgttacc ccacctgggt ggtactgtga tgagaattgg | 2400 |
| taatcatcgg ctgcagttat ggtgtagact ctgggcctgt cactgctgtc acatgtggct | 2460 |
| accatttttg ggtcaagccc tattgcgggg atggggtcac caagcctcac ataccaaga | 2520 |
| tcatatgatg tgggtaagct gaggacggtg accccttccc ctactaggac gttcccaatt | 2580 |
| ttgtcgttga tgttggctgt tgcagacatc aaccattgt agctaacatc tgtcagttca | 2640 |
| ctcaggcttc ctggaagggt cacggcggtt atggtgccgt ttagtgcata aacgccacca | 2700 |
| ggaagtgtgc ttgacctcac tgtgagactc cgactcacta gcctgcagta gttgtaactg | 2760 |
| gccggtaggt tctgggcagt caggagcatc tgatcgaact ttagttccc attgccctgc | 2820 |
| agtgtgtagt gagcaccac aattgagcca gggaatccag ggaaaaagac aattagccct | 2880 |
| gaccctgtgt ccccccagct caaattgtag gtcgaggtct ctgacctgag agtgtgcttc | 2940 |
| tccagggtgt cgtccggaat ggacgccggt ccggttggtg gcatcagaag gctccgtatg | 3000 |

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| | |
|---|------|
| aacggaacaa tctgctgggt ttgatctgac aggtttgtca tcgatgcgat cgaattccgc | 3060 |
| gcgcttcgga ccgggatccg cgcccgatgg tgggacggta tgaataatcc ggaatattta | 3120 |
| taggtttttt tattacaaaa ctgttacgaa aacagtaaaa tacttattta tttgcgagat | 3180 |
| ggttatcatt ttaattatct ccatgatcta ttaatattcc ggagtatacg gacctttaat | 3240 |
| tcaaccaaac acaatatatt atagttaa atagaattatt atcaaatacat ttgtatatta | 3300 |
| attaaaatac tatactgtaa attacatttt atttacaatc actcgacgaa gacttgatca | 3360 |
| cccgggatct cgaggctgac ggtatcg atg agt gac gtt ttc aat agt cca cag | 3414 |
| Met Ser Asp Val Phe Asn Ser Pro Gln | |
| 1 5 | |
| gcg cga agc acg atc tca gca gcg ttc ggc ata aag cct act gct gga | 3462 |
| Ala Arg Ser Thr Ile Ser Ala Ala Phe Gly Ile Lys Pro Thr Ala Gly | |
| 10 15 20 25 | |
| caa gac gtg gaa gaa ctc ttg atc cct aaa gtt tgg gtg cca cct gag | 3510 |
| Gln Asp Val Glu Glu Leu Leu Ile Pro Lys Val Trp Val Pro Pro Glu | |
| 30 35 40 | |
| gat ccg ctt gcc agc cct agt cga ctg gca aag ttc ctc aga gag aac | 3558 |
| Asp Pro Leu Ala Ser Pro Ser Arg Leu Ala Lys Phe Leu Arg Glu Asn | |
| 45 50 55 | |
| ggc tac aaa gtt ttg cag ccg cgg tct ctg ccc gag aat gag gag tat | 3606 |
| Gly Tyr Lys Val Leu Gln Pro Arg Ser Leu Pro Glu Asn Glu Glu Tyr | |
| 60 65 70 | |
| gag acc gac caa ata ctc cca gac tta gca tgg atg cga cag ata gaa | 3654 |
| Glu Thr Asp Gln Ile Leu Pro Asp Leu Ala Trp Met Arg Gln Ile Glu | |
| 75 80 85 | |
| ggg gct gtt tta aaa ccc act cta tct ctc cct att gga gat cag gag | 3702 |
| Gly Ala Val Leu Lys Pro Thr Leu Ser Leu Pro Ile Gly Asp Gln Glu | |
| 90 95 100 105 | |
| tac ttc cca aag tac tac cca aca cat cgc cct agc aag gag aag ccc | 3750 |
| Tyr Phe Pro Lys Tyr Tyr Pro Thr His Arg Pro Ser Lys Glu Lys Pro | |
| 110 115 120 | |
| aat gcg tac cca cca gac atc gca cta ctc aag cag atg att tac ctg | 3798 |
| Asn Ala Tyr Pro Pro Asp Ile Ala Leu Leu Lys Gln Met Ile Tyr Leu | |
| 125 130 135 | |
| ttt ctc cag gtt cca gag gcc aac gag ggc cta aag gat gaa gta acc | 3846 |
| Phe Leu Gln Val Pro Glu Ala Asn Glu Gly Leu Lys Asp Glu Val Thr | |
| 140 145 150 | |
| ctc ttg acc caa aac ata agg gac aag gcc tat gga agt ggg acc tac | 3894 |
| Leu Leu Thr Gln Asn Ile Arg Asp Lys Ala Tyr Gly Ser Gly Thr Tyr | |
| 155 160 165 | |
| atg gga caa gca aat cga ctt gtg gcc atg aag gag gtc gcc act gga | 3942 |
| Met Gly Gln Ala Asn Arg Leu Val Ala Met Lys Glu Val Ala Thr Gly | |
| 170 175 180 185 | |
| aga aac cca aac aag gat cct cta aag ctt ggg tac act ttt gag agc | 3990 |
| Arg Asn Pro Asn Lys Asp Pro Leu Lys Leu Gly Tyr Thr Phe Glu Ser | |
| 190 195 200 | |

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| | |
|---|------|
| atc gcg cag cta ctt gac atc aca cta ccg gta ggc cca ccc ggt gag Ile Ala Gln Leu Leu Asp Ile Thr Leu Pro Val Gly Pro Pro Gly Glu 205 210 215 | 4038 |
| gat gac aag ccc tgg gtg cca ctc aca aga gtg ccg tca cgg atg ttg Asp Asp Lys Pro Trp Val Pro Leu Thr Arg Val Pro Ser Arg Met Leu 220 225 230 | 4086 |
| gtg ctg acg gga gac gta gat ggc gac ttt gag gtt gaa gat tac ctt Val Leu Thr Gly Asp Val Asp Gly Asp Phe Glu Val Glu Asp Tyr Leu 235 240 245 | 4134 |
| ccc aaa atc aac ctc aag tca tca agt gga cta cca tat gta ggt cgc Pro Lys Ile Asn Leu Lys Ser Ser Gly Leu Pro Tyr Val Gly Arg 250 255 260 265 | 4182 |
| acc aaa gga gag aca att ggc gag atg ata gct ata tca aac cag ttt Thr Lys Gly Glu Thr Ile Gly Glu Met Ile Ala Ile Ser Asn Gln Phe 270 275 280 | 4230 |
| ctc aga gag cta tca aca ctg ttg aag caa ggt gca ggg aca aag ggg Leu Arg Glu Leu Ser Thr Leu Leu Lys Gln Gly Ala Gly Thr Lys Gly 285 290 295 | 4278 |
| tca aac aag aag aag cta ctc agc atg tta agt gac tat tgg tac tta Ser Asn Lys Lys Lys Leu Leu Ser Met Leu Ser Asp Tyr Trp Tyr Leu 300 305 310 | 4326 |
| tca tgc ggg ctt ttg ttt cca aag gct gaa agg tac gac aaa agt aca Ser Cys Gly Leu Leu Phe Pro Lys Ala Glu Arg Tyr Asp Lys Ser Thr 315 320 325 | 4374 |
| tgg ctc acc aag acc cgg aac ata tgg tca gct cca tcc cca aca cac Trp Leu Thr Lys Thr Arg Asn Ile Trp Ser Ala Pro Ser Pro Thr His 330 335 340 345 | 4422 |
| ctc atg atc tcc atg atc acc tgg ccc gtg atg tcc aac agc cca aat Leu Met Ile Ser Met Ile Thr Trp Pro Val Met Ser Asn Ser Pro Asn 350 355 360 | 4470 |
| aac gtg ttg aac att gaa ggg tgt cca tca ctc tac aaa ttc aac ccg Asn Val Leu Asn Ile Glu Gly Cys Pro Ser Leu Tyr Lys Phe Asn Pro 365 370 375 | 4518 |
| ttc aga gga ggg ttg aac agg atc gtc gag tgg ata ttg gcc ccg gaa Phe Arg Gly Gly Leu Asn Arg Ile Val Glu Trp Ile Leu Ala Pro Glu 380 385 390 | 4566 |
| gaa ccc aag gct ctt gta tat gcg gac aac ata tac att gtc cac tca Glu Pro Lys Ala Leu Val Tyr Ala Asp Asn Ile Tyr Ile Val His Ser 395 400 405 | 4614 |
| aac acg tgg tac tca att gac cta gag aag ggt gag gca aac tgc act Asn Thr Trp Tyr Ser Ile Asp Leu Glu Lys Gly Glu Ala Asn Cys Thr 410 415 420 425 | 4662 |
| cgc caa cac atg caa gcc gca atg tac tac ata ctc acc aga ggg tgg Arg Gln His Met Gln Ala Ala Met Tyr Tyr Ile Leu Thr Arg Gly Trp 430 435 440 | 4710 |
| tca gac aac ggc gac cca atg ttc aat caa aca tgg gcc acc ttt gcc Ser Asp Asn Gly Asp Pro Met Phe Asn Gln Thr Trp Ala Thr Phe Ala 4758 | |

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| 445 | 450 | 455 | |
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| atg aac att gcc cct gct cta gtg Met Asn Ile Ala Pro Ala Leu Val | gtg gac tca tcg tgc ctg ata atg Val Asp Ser Ser Cys Leu Ile Met | 4806 | |
| aac ctg caa att aag acc tat ggt Asn Leu Gln Ile Lys Thr Tyr | caa ggc agc ggg aat gca gcc acg Gln Gly Ser Gly Asn Ala Ala Thr | 4854 | |
| ttc atc aac aac cac ctc ttg agc Phe Ile Asn Asn His Leu Leu Ser | acg cta gtg ctt gac cag tgg aac Thr Leu Val Leu Asp Gln Trp Asn | 4902 | |
| ttg atg aga cag ccc aga cca gac Leu Met Arg Gln Pro Arg Pro Asp | agc gag gag ttc aaa tca att gag Ser Thr Leu Val Leu Phe Lys Ser Ile Glu | 4950 | |
| gac aag cta ggt atc aac ttt aag Asp Lys Leu Gly Ile Asn Phe Lys | att gag agg tcc att gat gat atc Ile Glu Arg Ser Ile Asp Asp Ile | 4998 | |
| agg ggc aag ctg aga cag ctt gtc Arg Gly Lys Leu Arg Gln Leu Val | ctc ctt gca caa cca ggg tac ctg Leu Leu Ala Gln Pro Gly Tyr Leu | 5046 | |
| agt ggg ggg gtt gaa cca gaa caa Ser Gly Gly Val Glu Pro Glu Gln | tcc agc cca act gtt gag ctt gac Ser Ser Pro Thr Val Glu Leu Asp | 5094 | |
| cta cta ggg tgg tca gct aca tac Leu Leu Gly Trp Ser Ala Thr Tyr | agc aaa gat ctc ggg atc tat gtg Ser Lys Asp Leu Gly Ile Tyr Val | 5142 | |
| ccg gtg ctt gac aag gaa cgc cta Pro Val Leu Asp Lys Glu Arg Leu | ttt tgt tct gct gcg tat ccc aag Phe Cys Ser Ala Tyr Pro Lys | 5190 | |
| gga gta gag aac aag agt ctc aag Gly Val Glu Asn Lys Ser Leu Lys | tcc aaa gtc ggg atc gag cag gca Ser Lys Val Gly Ile Glu Gln Ala | 5238 | |
| tac aag gta gtc agg tat gag gcg Tyr Lys Val Val Arg Tyr Glu Ala | tta agg ttg gta ggt ggt tgg aac Leu Arg Leu Val Gly Gly Trp Asn | 5286 | |
| tac cca ctc ctg aac aaa gcc tgc Tyr Pro Leu Leu Asn Lys Ala Cys | aag aat aac gca ggc gcc gct cgg Lys Asn Asn Ala Gly Ala Ala Arg | 5334 | |
| cgg cat ctg gag gcc aag ggg ttc Arg His Leu Glu Ala Lys Gly Phe | cca ctc gac gag ttc cta gcc gag Pro Leu Asp Glu Phe Leu Ala Glu | 5382 | |
| tgg tct gag ctg tca gag ttc ggt Trp Ser Glu Leu Ser Glu Phe Gly | gag gcc ttc gaa ggc ttc aat atc Glu Phe Glu Gly Phe Asn Ile | 5430 | |
| aag ctg acc gta aca tct gag agc Lys Leu Thr Val Thr Ser Glu Ser | cta gcc gaa ctg aac aag cca gta Leu Ala Glu Leu Asn Lys Pro Val | 5478 | |
| ccc ccc aag ccc cca aat gtc aac aga cca gtc aac act ggg gga ctc | | 5526 | |

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|------------|-------------|------------|------------|------------|------------|-----|------------|------------|------------|-----|-----|-----|-----|-----|-----|------|
| Pro | Pro | Lys | Pro | Pro | Asn | Val | Asn | Arg | Pro | Val | Asn | Thr | Gly | Gly | Leu | |
| | | 700 | | | | | 705 | | | | | 710 | | | | |
| aag | gca | gtc | agc | aac | gcc | ctc | aag | acc | ggt | cgg | tac | agg | aac | gaa | gcc | 5574 |
| Lys | Ala | Val | Ser | Asn | Ala | Leu | Lys | Thr | Gly | Arg | Tyr | Arg | Asn | Glu | Ala | |
| | 715 | | | | | 720 | | | | | 725 | | | | | |
| gga | ctg | agt | ggt | ctc | gtc | ctt | cta | gcc | aca | gca | aga | agc | cgt | ctg | caa | 5622 |
| Gly | Leu | Ser | Gly | Leu | Val | Leu | Leu | Ala | Thr | Ala | Arg | Ser | Arg | Leu | Gln | |
| | 730 | | | | 735 | | | | | 740 | | | | | 745 | |
| gat | gca | gtt | aag | gcc | aag | gca | gaa | gcc | gag | aaa | ctc | cac | aag | tcc | aag | 5670 |
| Asp | Ala | Val | Lys | Ala | Lys | Ala | Glu | Ala | Glu | Lys | Leu | His | Lys | Ser | Lys | |
| | | | | 750 | | | | | 755 | | | | | 760 | | |
| cca | gac | gac | ccc | gat | gca | gac | tgg | ttc | gaa | aga | tca | gaa | act | ctg | tca | 5718 |
| Pro | Asp | Asp | Pro | Asp | Ala | Asp | Trp | Phe | Glu | Arg | Ser | Glu | Thr | Leu | Ser | |
| | | | 765 | | | | | 770 | | | | | 775 | | | |
| gac | ctt | ctg | gag | aaa | gcc | gac | atc | gcc | agc | aag | gtc | gcc | cac | tca | gca | 5766 |
| Asp | Leu | Leu | Glu | Lys | Ala | Asp | Ile | Ala | Ser | Lys | Val | Ala | His | Ser | Ala | |
| | | 780 | | | | | 785 | | | | | 790 | | | | |
| ctc | gtg | gaa | aca | agc | gac | gcc | ctt | gaa | gca | gtt | cag | tcg | act | tcc | gtg | 5814 |
| Leu | Val | Glu | Thr | Ser | Asp | Ala | Leu | Glu | Ala | Val | Gln | Ser | Thr | Ser | Val | |
| | 795 | | | | | 800 | | | | | 805 | | | | | |
| tac | acc | ccc | aag | tac | cca | gaa | gtc | aag | aac | cca | cag | acc | gcc | tcc | aac | 5862 |
| Tyr | Thr | Pro | Lys | Tyr | Pro | Glu | Val | Lys | Asn | Pro | Gln | Thr | Ala | Ser | Asn | |
| | | | | | 815 | | | | | 820 | | | | | 825 | |
| ccg | gtt | gtt | ggg | ctc | cac | ctg | ccc | gcc | aag | agg | gcc | acc | ggt | gtc | cag | 5910 |
| Pro | Val | Val | Gly | Leu | His | Leu | Pro | Ala | Lys | Arg | Ala | Thr | Gly | Val | Gln | |
| | | | | 830 | | | | | 835 | | | | | 840 | | |
| gcc | gct | ctt | ctc | gga | gca | gga | acg | agc | aga | cca | atg | ggg | atg | gag | gcc | 5958 |
| Ala | Ala | Leu | Leu | Gly | Ala | Gly | Thr | Ser | Arg | Pro | Met | Gly | Met | Glu | Ala | |
| | | | 845 | | | | | 850 | | | | 855 | | | | |
| cca | aca | cgg | tcc | aag | aac | gcc | gtg | aaa | atg | gcc | aaa | cgg | cgg | caa | cgc | 6006 |
| Pro | Thr | Arg | Ser | Lys | Asn | Ala | Val | Lys | Met | Ala | Lys | Arg | Arg | Gln | Arg | |
| | | 860 | | | | | 865 | | | | | 870 | | | | |
| caa | aag | gag | agc | cgc | caa | tag | ccatgaggcg | gccctgatgc | atagcatgcg | | | | | | | 6057 |
| Gln | Lys | Glu | Ser | Arg | Gln | | | | | | | | | | | |
| | 875 | | | | | | | | | | | | | | | |
| gtaccgggag | atgggggagg | ctaactgaaa | cacggaagga | gacaataccg | gaaggaaccc | | | | | | | | | | | 6117 |
| gcgctatgac | ggcaataaaa | agacagaata | aaacgcacgg | gtgttgggtc | gtttgttcat | | | | | | | | | | | 6177 |
| aaacgcgggg | ttcgggtccca | gggctggcac | tctgtcgata | ccccaccgag | acccattgg | | | | | | | | | | | 6237 |
| gaccaatacg | cccgcgtttc | ttccttttcc | ccaccccaac | cccgaagttc | gggtgaaggc | | | | | | | | | | | 6297 |
| ccagggctcg | cagccaacgt | cggggcggca | agccctgcc | tagccactac | gggtacgtag | | | | | | | | | | | 6357 |
| gccaaccact | agaactatag | ctagagtcct | gggcgaacaa | acgatgctcg | ccttcagaa | | | | | | | | | | | 6417 |
| aaccgaggat | gcgaaccact | tcatccgggg | tcagcaccac | cggcaagcgc | cgcgacggcc | | | | | | | | | | | 6477 |
| gaggtctacc | gatctcctga | agccagggca | gatccgtgca | cagcaccttg | ccgtagaaga | | | | | | | | | | | 6537 |

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|------------|------------|-------------|-------------|-------------|-------------|------|
| acagcaaggc | cgccaatgcc | tgacgatgcg | tgagagaccga | aaccttgcg | tcgttcgcca | 6597 |
| gccaggacag | aaatgcctcg | acttcgctgc | tgcccaagggt | tgccgggtga | cgcacaccgt | 6657 |
| ggaaacggat | gaaggcacga | accagttga | cataagcctg | ttcggttcgt | aaactgtaat | 6717 |
| gcaagtagcg | tatgcgtca | cgcaactgg | ccagaacctt | gaccgaacgc | agcggtggt | 6777 |
| acggcgagc | ggcggttttc | atggcttggt | atgactgttt | ttttgtacag | tctatgcctc | 6837 |
| gggcatccaa | gcagcaagcg | cgttacgccg | tggtcgatg | tttgatgtta | tgagcagca | 6897 |
| acgatgttac | gcagcagcaa | cgatgttacg | cagcagggca | gtcgccctaa | aacaaagtta | 6957 |
| ggtggctcaa | gtatgggcat | cattcgaca | tgtaggctcg | gccctgacca | agtcaaattcc | 7017 |
| atgcgggctg | ctcttgatct | tttcggtcgt | gagttcggag | acgtagccac | ctactcccaa | 7077 |
| catcagccgg | actccgatta | cctcgggaac | ttgctccgta | gtaagacatt | catcgcgctt | 7137 |
| gctgccttcg | accaagaagc | ggttggtggc | gctctcgcg | cttacgttct | gcccaggttt | 7197 |
| gagcagccgc | gtagtgaat | ctatatctat | gatctcgag | tctccggcga | gcaccggagg | 7257 |
| cagggcattg | ccaccgcgt | catcaatctc | ctcaagcatg | aggccaacgc | gcttggtgct | 7317 |
| tatgtgatct | acgtgcaagc | agattacggt | gacgatcccg | cagtggctct | ctatacaaag | 7377 |
| ttgggcatac | gggaagaagt | gatgcacttt | gatatcgacc | caagtaccgc | cacctaacaa | 7437 |
| ttcgttcaag | ccgagatcgg | cttcccggcc | gcggagttgt | tcggtaaatt | gtcacaacgc | 7497 |
| cgcaatata | gtctttacca | tgcccttggc | cacgcccctc | tttaatacga | cgggcaattt | 7557 |
| gcacttcaga | aaatgaagag | tttgcttttag | ccataacaaa | agtccagtat | gctttttcac | 7617 |
| agcataactg | gactgatttc | agtttacaac | tattctgtct | agtttaagac | tttattgtca | 7677 |
| tagtttagat | ctattttggt | cagtttaaga | ctttattgtc | cgccacacc | cgcttacgca | 7737 |
| gggcatccat | ttattactca | accgtaaccg | atgttgccag | gttacgcggc | tggtctgcgg | 7797 |
| tgtgaaatac | cgcacagatg | cgtaaggaga | aaataccgca | tcaggcgctc | ttccgcttcc | 7857 |
| tcgctcactg | actcgctgcg | ctcggtcggt | cggctgcggc | gagcgggtatc | agctcactca | 7917 |
| aaggcggtaa | tacggttatc | cacagaatca | ggggataacg | caggaaagaa | catgtgagca | 7977 |
| aaaggccagc | aaaaggccag | gaaccgtaaa | aaggccgcgt | tgctggcggt | tttccatagg | 8037 |
| ctccgcccc | ctgacgagca | tcacaaaaat | cgacgctcaa | gtcagagggtg | gcgaaacccg | 8097 |
| acaggactat | aaagatacca | ggcgtttccc | cctggaagct | ccctcgctgcg | ctctcctggt | 8157 |
| ccgaccctgc | cgcttaccgg | atacctgtcc | gcctttctcc | cttcgggaag | cgtaggcgctt | 8217 |
| tctcaatgct | cacgctgtag | gtatctcagt | tcggtgtagg | tcgttcgctc | caagctgggc | 8277 |
| tgtgtgcacg | aacccccgt | tcagcccgac | cgctgcgcct | tatccggtaa | ctatcgtctt | 8337 |
| gagtccaacc | cggtaagaca | cgacttatcg | ccactggcag | cagccactgg | taacaggatt | 8397 |
| agcagagcga | ggtatgtagg | cggtgctaca | gagttcttga | agtgggtggcc | taactacggc | 8457 |

114 Sequence Listing.ST25.txt

| | | | | | | |
|------------|------------|-------------|-------------|------------|-------------|-------|
| tacactagaa | ggacagtatt | tggtatctgc | gctctgctga | agccagttac | cttcggaaaa | 8517 |
| agagttggta | gctcttgatc | cggcaaacaa | accaccgctg | gtagcgggtg | tttttttggt | 8577 |
| tgcaagcagc | agattacgcg | cagaaaaaaaa | ggatctcaag | aagatccttt | gatcttttct | 8637 |
| acggggtctg | acgctcagt | gaacgaaaac | tcacgttaag | ggattttggt | catgagatta | 8697 |
| tcaaaaagga | tcttcaccta | gatcctttta | aattaaataat | gaagttttta | atcaatctaa | 8757 |
| agtatatatg | agtaaacttg | gtctgacagt | taccaatgct | taatcagtga | ggcacctatc | 8817 |
| tcagcgatct | gtctatttcg | ttcatccata | gttgccctgac | tccccgtcgt | gtagataact | 8877 |
| acgatacggg | agggttacc | atctggcccc | agtgtgcaa | tgataccgcg | agaccacgc | 8937 |
| tcaccggctc | cagatttatc | agcaataaac | cagccagccg | gaagggccga | gcgcagaagt | 8997 |
| ggtcctgcaa | ctttatccgc | ctccatccag | tctattaatt | gttgccggga | agctagagta | 9057 |
| agtagttcgc | cagttaatag | tttgcgcaac | gttggttgcca | ttgctacagg | catcgtgggtg | 9117 |
| tcacgctcgt | cgtttggtat | ggcttcattc | agctccggtt | cccaacgatc | aaggcgagtt | 9177 |
| acatgatccc | ccatgttgtg | caaaaaagcg | gttagctcct | tcggtcctcc | gatcgttgtc | 9237 |
| agaagtaagt | tgccgcagc | gttatcactc | atggttatgg | cagcactgca | taattctctt | 9297 |
| actgtcatgc | catccgtaag | atgcttttct | gtgactgggtg | agtactcaac | caagtcattc | 9357 |
| tgagaatagt | gtatgcggcg | accgagttgc | tcttgcccgg | cgtcaatacg | ggataatacc | 9417 |
| gcgccacata | gcagaacttt | aaaagtgtc | atcattggaa | aacgttcttc | ggggcgaaaa | 9477 |
| ctctcaagga | tcttaccgct | gttgagatcc | agttcgatgt | aaccactcg | tgcacccaac | 9537 |
| tgatcttcag | catcttttac | tttcaccagc | gtttctgggt | gagcaaaaac | aggaaggcaa | 9597 |
| aatgccgcaa | aaaagggaat | aagggcgaca | cggaaatgtt | gaatactcat | actcttcctt | 9657 |
| tttcaatatt | attgaagcat | ttatcagggt | tattgtctca | tgagcggata | catatttgaa | 9717 |
| tgtatttaga | aaaataaaca | aataggggtt | ccgcgcacat | ttccccgaaa | agtgccacct | 9777 |
| gaaattgtaa | acgttaatat | tttgttaaaa | ttcgcgttaa | atttttgtta | aatcagctca | 9837 |
| ttttttaacc | aataggccga | aatcggcaaa | atcccttata | aatcaaaaga | atagaccgag | 9897 |
| atagggttga | gtgttggtcc | agtttggaac | aagagtccac | tattaaagaa | cgtggactcc | 9957 |
| aacgtcaaag | ggcgaaaaac | cgtctatcag | ggcgatggcc | cactacgtga | accatcacc | 10017 |
| taatcaagtt | ttttggggtc | gaggtgccgt | aaagcactaa | atcggaaccc | taaaggagc | 10077 |
| ccccgattta | gagcttgacg | gggaaagccg | gcgaacgtgg | cgagaaagga | agggaagaaa | 10137 |
| gcgaaaggag | cgggcgctag | ggcgctggca | agtgtagcgg | tcacgctgcg | cgtaaccacc | 10197 |
| acaccgcgcg | cgcttaatgc | gccgctacag | ggcgctccc | attcgccatt | caggctgcaa | 10257 |
| ataagcgttg | atattcagtc | aattacaaac | attaataacg | aagagatgac | agaaaaattt | 10317 |

114 Sequence Listing.ST25.txt

```
tcattctgtg acagagaaaa agtagccgaa gatgacggtt tgtcacatgg agttggcagg 10377
atgtttgatt aaaaacataa caggaagaaa aatgccccgc tgtgggcgga caaaatagtt 10437
gggaactggg aggggtggaa atggagtttt taaggattat ttagggaaga gtgacaaaat 10497
agatgggaac tgggtgtagc gtcgtaagct aatacgaaaa ttaaaaatga caaaatagtt 10557
tggaactaga tttcacttat ctggttcgga tctcctaggc tcaagcagtg atcagatcca 10617
gacatgataa gatacattga tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaaa 10677
tgctttattt gtgaaatttg tgatgctatt gctttatttg taaccattat aagctgcaat 10737
aaacaagtta acaacaacaa ttgcattcat tttatgtttc aggttcaggg ggaggtgtgg 10797
gaggtttttt aaagcaagta aaacctctac aaatgtggta tggctgatta tgatcctcta 10857
gtacttctcg acaagcttgt cgagactgca ggctctagat tcgaaagcgg cc 10909
```

<210> 2
 <211> 879
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 2

Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
 1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
 35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
 50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125

114 Sequence Listing.ST25.txt

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu
165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
225 230 235 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
245 250 255

Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
260 265 270

Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu
275 280 285

Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
290 295 300

Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
305 310 315 320

Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
325 330 335

Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
340 345 350

Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
355 360 365

Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
370 375 380

114 Sequence Listing.ST25.txt

Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr
385 390 395 400

Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
405 410 415

Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
420 425 430

Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
435 440 445

Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
450 455 460

Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
465 470 475 480

Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
485 490 495

Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro
500 505 510

Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
515 520 525

Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
530 535 540

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
545 550 555 560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
565 570 575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
580 585 590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
595 600 605

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
625 630 635 640

114 Sequence Listing.ST25.txt

Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 3

114 Sequence Listing.ST25.txt

<211> 13
 <212> PRT
 <213> Infectious bursal disease virus
 <400> 3

Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu Glu
 1 5 10

<210> 4
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 4
 gggggaattc atggcatcag agttcaaaga gaccccc

37

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 5
 cgcgggtacc ttaccagcgg ccagccgac c

31

<210> 6
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6
 cgcgggtacc ttaaccaggg ggtctctgtg ttg

33

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 7
 cgcgggtacc ttatgttgga gcattgggtt ttg

33

<210> 8
 <211> 31
 <212> DNA
 <213> Artificial Sequence

114 Sequence Listing.ST25.txt

<220>

<223> Synthetic Construct

<400> 8

cgcggtacc ttattttggc ttgggctttg g

31

<210> 9

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 9

cgcggtacc ttatggtaga gcccgcctgg g

31